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Cannibalism Stress Response in Bacillus subtilis

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Cannibalism Stress Response in *Bacillus subtilis*

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Abstract

When faced with carbon source limitation, the Gram-positive soil organism *Bacillus subtilis* initiates a survival strategy called sporulation, which leads to the formation of highly resistant endospores that allow *B. subtilis* to survive even long periods of starvation. In order to avoid commitment to this energy-demanding and irreversible process, *B. subtilis* employs another strategy called cannibalism to delay sporulation as long as possible. Cannibalism involves the production and secretion of two cannibalism toxins, the sporulation delaying protein, SDP, and the sporulation killing factor, SKF, which are able to lyse sensitive siblings. The lysed cells are thought to then provide nutrients for the cannibals to slow down or even prevent them from entering sporulation. In this study, we uncovered the role of the cell envelope stress response (CESR), especially the Bce-like antimicrobial peptide detoxification modules, in cannibalism stress response during stationary phase. SDP and SKF specifically induce Bce-like systems and some ECF σ factors in stationary phase cultures, but only the latter provide some degree of protection. A full Bce response is only triggered by mature toxins, but not by toxin precursors. Our study provides insights into the close relationship between stationary phase survival and the CESR of *B. subtilis*. [**199 words]**

Introduction

In their natural environment, microorganisms constantly compete for nutrients. In order to defend their habitat against invading species, many bacteria produce and secrete antimicrobial peptides (AMPs) that interfere with the integrity or biosynthesis of the cell envelope. AMP action leads to an arrest in cell growth and often to cell lysis (Silver, 2003; Silver, 2006; Walsh, 2003). To defend against such antimicrobial attacks, many bacteria induce a complex cell envelope stress response (CESR). In *Bacillus subtilis*, the underlying regulatory network is orchestrated by four two-component systems (TCS) and seven extracytoplasmic function (ECF) σ factors (Helmann, 2002; Jordan *et al.*, 2007; Schrecke *et al.*, 2012).

While it is generally accepted that the CESR network has evolved to maintain envelope integrity in the face of AMPs produced by competing species, little is known about the extent to which it is also involved in responding to endogenously produced AMPs. For instance, although it is known that the AMPs are co-expressed with dedicated immunity proteins that prevent cells from autolysis (Dubois *et al.*, 2009; Ellermeier *et al.*, 2006; Gonzalez-Pastor *et al.*, 2003), it is conceivable that the level of self-protection via these mechanisms can be insufficient, raising the need for additional protection by the CESR network. In fact, we recently reported that in early stationary phase a subpopulation of *B. subtilis* cells strongly induces one of the CESR modules, the LiaRS system, even in the absence of competitors and without any external addition of AMPs (Dominguez-Escobar *et al.*, 2014; Jordan *et al.*, 2007). Here, we set out to test whether other systems of the CESR network of *B. subtilis* also displayed such an intrinsic induction behavior during stationary phase and, if so, whether this was causally related to the endogenous production of AMPs.

To study these questions, we focused on the expression of the core of the CESR network, comprising the AMP-resistance modules, BceRS and PsdRS, as well as the ECF σ factors σ^M, σ^X and σ^W. While the BceRS and PsdRS systems regulate ABC transporters (BceAB and PsdAB, respectively) that specifically confer resistance against a number of AMPs (Staroń *et al.*, 2011), the regulons of the ECF σ factors are known to play a more promiscuous role in cell envelope stress response to antimicrobial compounds (Helmann, 2002; Kingston *et al.*, 2013; Mascher *et al.*, 2007; Missiakas & Raina, 1998). σ^M, σ^X and σ^W each regulate a set of about 30-60 target genes with partially overlapping specificity (Kingston *et al.*, 2013; Mascher *et al.*, 2007), and all are activated in a growth-phase and growth medium-dependent manner (Huang *et al.*, 1998): While σ^M and σ^X are induced mainly in late logarithmic growth phase, σ^W only becomes active in early stationary phase (Huang *et al.*, 1998; Nicolas *et al.*, 2012).

So far, no growth phase dependency has been observed for the BceRS and PsdRS modules. Both systems respond to and mediate resistance against a variety of peptide antibiotics: The BceRS system responds to the cyclic peptide antibiotic bacitracin and to a lesser extent also to the lantibiotics actagardine and mersacidin (Mascher *et al.*, 2003; Rietkötter *et al.*, 2008), while the PsdRS system responds primarily to lantibiotics, such as nisin or gallidermin (Staroń *et al.*, 2011). Since the *B. subtilis* strain W168 is known to produce and secrete a variety of similar AMPs, it was conceivable that they might also act as inducers of the BceRS and PsdRS modules.

In this study, we show that the BceRS and PsdRS system are, in fact, intrinsically activated during stationary phase growth of *B. subtilis*, and single out the inducers amongst a number of endogenously produced AMP candidates. The biological role of these AMPs has previously been implicated in a process termed "cannibalism", in which the stationary phase population bifurcates into a fraction of AMP-producing cells that feed on another fraction of non-producing cells (Chung *et al.*, 1994; Gonzalez-Pastor *et al.*, 2003). Our data reveals that the CESR network not only serves as a defense against extrinsic attacks from competing species, but also plays a novel role in the intrinsic cannibalism stress response. Interestingly, we show that activation of the BceRS and PsdRS modules by cannibalism toxins critically hinges on the presence of the cognate immunity proteins, providing further insight into the mode of stimulus perception by these systems. **[709 words]**

Methods

Media and growth conditions. *B. subtilis* and *E. coli* were routinely grown in Luria-Bertani (LB) medium or MCSE (Radeck *et al.*, 2013) including 0.2% fructose (w/v) as C-source at 37°C with agitation. The final composition of MCSE is as follows: 1× MOPS (from 10× MOPS buffer: 83.72 g l^{-1} MOPS, 33 g l^{-1} $(NH_4)_2SO_4$, 3.85 mM KH_2PO_4, 6.15 mM K_2HPO_4; adjusted to pH 7 with KOH), 50 mg l^{-1} Tryptophan, 22 mg l^{-1} ammonium ferric

citrate, 1× III'-salts (232 mg l^{-1} $MnSO_4x4H_2O$, 12.3 g l^{-1} $MgSO_4x7H_2O$), 0.8% (w/v) K-glutamate, 0.6% (w/v) Na-succinate, 0.2% (w/v) fructose. MCSE results in well-defined growth behavior and supports sporulation of *B. subtilis* under the growth conditions applied. Selective media for *B. subtilis* contained chloramphenicol (5 µg ml^{-1}), kanamycin (10 µg ml^{-1}), spectinomycin (100 µg ml^{-1}), or erythromycin (1 µg ml^{-1}) plus lincomycin (25 µg ml^{-1}) for macrolide-lincosamide-streptogramin B (MLS) resistance. Selective media for *E. coli* contained ampicillin (100 µg ml^{-1}) or chloramphenicol (35 µg ml^{-1}). Solid media additionally contained 1.5% (w/v) agar.

Bacterial strains and plasmids. Transcriptional promoter fusions to bacterial luciferase (*luxABCDE*) were constructed in pAH328 (Schmalisch *et al.*, 2010) or the pAH328 derivative pBS3Clux (Radeck *et al.*, 2013) using *Not*I/*Sal*I or *Eco*RI/*Spe*I restriction enzymes, respectively. All strains used in this study are listed in Table 1. All *B. subtilis* strains in this study are derivatives of the laboratory wild type strain W168. All plasmids and oligonucleotides are listed in Table 2 and 3, respectively.

DNA manipulations. All plasmids were constructed by standard cloning techniques and ligation mixtures were transformed into *E. coli* competent cells (DH5α, XL1-blue). The plasmids were verified by sequencing and transformed into *B. subtilis* as described previously (Harwood & Cutting, 1990). Plasmid integration into the *B. subtilis* chromosome was checked by colony-PCR. Preparation of chromosomal DNA from *B. subtilis* for transformation was prepared according to standard procedure (Cutting & Van der Horn, 1990).

Allelic replacement mutagenesis of *sdpAB, sdpC, sdpI, skfA-H, skfA, skfBC, skfEF, skfGH, skfH, sunA and yydF-J* using LFH-PCR. Long Flanking Homology PCR (LFH-

PCR) technique was performed as described previously (Mascher *et al.*, 2003). The constructed strains are listed in Table 1 and the corresponding primers are listed in Table 3.

Luminescence Assay. Promoter activities were detected by following luminescence in a Synergy™2 multi-mode microplate reader from BioTek® (Winooski, VT, USA) using Gen5™ software. Strain cultivation was performed as follows: Freshly prepared and pre-warmed (37°C) MCSE medium was inoculated 1:500 from overnight cultures and incubated at 37°C with agitation until OD_{600} 0.2. The culture was subsequently diluted to an OD_{600} of 0.05 with MCSE and 100 µl were transferred to one well of a 96-well plate (black walls, clear bottom; Greiner Bio-One, Frickenhausen, Germany). OD_{600} and luminescence were recorded every ten minutes for 18 hours. Incubation was performed at 37°C with agitation (medium intensity). Raw luminescence data were normalized to cell density by dividing luminescence per OD_{600} at each data point (relative luminescence units (RLU) / OD_{600}). For each individual sample, OD_{600} and luminescence were background-corrected by subtracting the respective mean values measured for MCSE medium only and TMB1578 (pAH328 empty) over every time point. Subsequently, RLU/OD_{600} values were calculated for each measurement and mean values and SEM (standard error of the mean) were determined from at least three independent biological replicates. **[834 words]**

Results and Discussion

Intrinsic induction of CESR target promoters during stationary phase growth

Initially, we aimed at investigating if other modules within the CESR network displayed induction profiles similar to the LiaRS system, which – when grown into stationary phase – displayed a clear induction pattern in the absence of any external stimulus (Dominguez-Escobar *et al.*, 2014). To this end, we fused the target promoters of the BceRS system (P_{bceA}), of the PsdRS system (P_{psdA}) and selected target promoters of σ^M, σ^X, and σ^W (P_{ydaH}, P_{sigX}, and

P_{pspA}, respectively) and one promoter which is regulated by all three σ factors, P_{bcrC}, to a promoter-less *luxABCDE* reporter (Radeck *et al.*, 2013; Schmalisch *et al.*, 2010). The resulting promoter-*lux* fusions were integrated into the chromosome of *B. subtilis* W168 wild type cells. Automated incubation of the resulting reporter strains in a microplate reader revealed that all but the σ^W target promoter P_{pspA} displayed a marked increase in luminescence activity between two and four hours after the onset of stationary phase (Fig. 1; t=7-8 h). The amplitude of this intrinsic stationary phase induction was highest for the BceRS and PsdRS target promoters (both approx. 500-fold induction; Fig. 1a, b), but also the ECF target promoters displayed a 10-20-fold increase in promoter activity (Fig. 1d). From these observations, we conclude that large parts of the CESR network in *B. subtilis* perceive one or multiple stimuli that are endogenously produced between two to four hours after entry into stationary phase.

AMPs and cannibalism toxins induce CESR systems

Both the BceRS and PsdRS system have been shown to respond to different peptide antibiotics that interfere with the cell wall biosynthetic pathway during exponential growth (Breukink & de Kruijff, 2006; Staroń *et al.*, 2011). In order to elucidate the mechanism behind the observed intrinsic stationary phase activation, we asked whether it could be caused by endogenously produced antimicrobial peptides of *B. subtilis* W168. The first AMP we considered was Sublancin 168 (SunA), which is a SPβ prophage-derived bacteriocin described as an S-linked glycopeptide active against Gram-positive bacteria (Oman *et al.*, 2011). Its production is known to be repressed during exponential growth phase by the transcriptional regulators AbrB and Rok (Albano *et al.*, 2005; Strauch *et al.*, 2007). Another peptide that might trigger stationary phase induction of the CESR is the YydF peptide, which has been shown to be an endogenous inducer of the LiaRS system (Butcher *et al.*, 2007; Wolf *et al.*, 2010). Its production is also negatively controlled by AbrB during logarithmic growth

178 (Butcher *et al.*, 2007). Subtilosin A (SboA) is another bacteriocin produced by *B. subtilis*
179 W168. Although it is known to be transcriptionally regulated by AbrB and by the two-
180 component regulatory proteins ResDE (Nakano *et al.*, 2000; Strauch *et al.*, 2007), it has been
181 reported to be produced only under anaerobic growth conditions (Nakano *et al.*, 2000).
182 Indeed, we found the *sboA* promoter to be inactive over the whole time course under our
183 cultivation conditions (data not shown). The last two potential AMPs were the two
184 cannibalism toxins sporulation delaying protein, SdpC and sporulation killing factor, SkfA
185 (referred to as SDP and SKF hereafter).
186 To study the effect of the AMPs on the induction of the CESR network, we analyzed P_{bceA},
187 P_{psdA} and P_{bcrC} promoter activation in mutants deleted for each gene encoding the respective
188 antimicrobial peptides (Fig. 2). Deletion of *sunA* (Sublancin 168) had no effect on any
189 promoter activity and deletion of *yydF-J* only showed a minor effect on P_{bceA} promoter
190 activity. In contrast, *sdpC* and *skfA-H* mutants revealed the most prominent reduction in
191 luciferase activity for all three promoters tested. Deletion of *sdpC* resulted in an approx. 10-
192 fold reduced P_{bceA} activity (Fig. 2b, blue curve), and deletion of *skfA-H* decreased the activity
193 about 100-fold (Fig. 2b, green curve). The effect of an *sdpC* deletion on P_{psdA} induction was
194 moderate (about 3-fold decrease), but P_{psdA} activity was almost completely lost in a *skfA-H*
195 mutant (Fig. 2d). In contrast, P_{bcrC} activity was more strongly decreased in the *sdpC* mutant
196 (about 4-fold, Fig. 2f) than in the *skfA-H* deletion strain (max. 2-fold). Moreover, in an *sdpC*
197 *skfA-H* double mutant, stationary phase activity of P_{bceA} and P_{psdA} was fully abolished, while
198 P_{bcrC} still displayed mild induction. Hence, we could identify the two cannibalism toxins SDP
199 and SKF as strong inducers of all three CESR target promoters in stationary phase. While
200 induction of ECF σ factors was expected, given the described role in mounting a secondary
201 layer of defense against SDP (Butcher & Helmann, 2006) this is the first time that an intrinsic
202 growth phase-dependent induction has been observed for Bce-like systems. Since the effect
203 was most prominent for the *bceA* promoter, subsequent investigations of the cannibalism

stress response were restricted to the BceRS system alone, but key findings were also verified for the PsdRS system, demonstrating similar behavior (data not shown).

Toxin production correlates with P_{bceA} induction

We next tested how stationary phase induction of P_{bceA} was correlated with the activation of *sdpC* and *skfA* expression. SDP is under dual control of first its own promoter P_{sdpC} and second under the promoter driving the whole *sdpABC* operon P_{sdpA} (Fig. 3). We tested both promoter activities over the whole time course and found P_{sdpA} to be the stronger promoter under our cultivation conditions (data not shown). Therefore, we assumed that P_{sdpA} is the crucial promoter driving also expression of *sdpC*. Thus, we studied the luminescence activity from P_{sdpA}- and P_{skfA}-*luxABCDE* reporter fusions throughout growth of the W168 wild type strain to test correlation between SDP/SKF production and P_{bceA} induction (Fig. 4). P_{sdpA} was induced about 10-fold, while P_{skfA} displayed a 100-fold induction. While both the *sdpA* and *skfA* promoters were induced 5-6 h after the beginning of the experiment, the *bceA* promoter became active approx. 2 h later. This indicates that the toxins first had to be produced, processed and likely also accumulated to a certain threshold concentration in order to activate the BceRS system.

The BceRS system does not mediate resistance against cannibalism toxins

Based on its role in mediating resistance against the peptide antibiotic bacitracin, we reasoned that the BceRS system might also confer resistance against SDP. The immunity protein of the *sdpABC-sdpRI* operon is SdpI (Fig. 3). Both the toxin biosynthesis operon *sdpABC* and the immunity operon *sdpRI* are under control of the transition state repressor AbrB and the master regulator of sporulation Spo0A (Ellermeier *et al.*, 2006). SdpI reveals receptor/signal transducing properties, and its synthesis is induced by a combined interplay between SDP, SdpI and SdpR (Ellermeier *et al.*, 2006). In brief, SdpR constitutes an autorepressor blocking

transcription of *sdpRI* in the absence of SDP. Upon SDP synthesis and export, SDP binds to SdpI at the membrane, which enables the latter to recruit SdpR into the SDP-SdpI membrane complex. This titration of SdpR away from the DNA induces transcription of *sdpRI*, which results in immunity against SDP (Ellermeier *et al.*, 2006). Accordingly, cannibalism-inactive cells are expected to neither produce and secrete SDP nor induce enhanced SdpI expression. Consequently, it is believed that these cells are highly sensitive to SDP and prone to lysis while toxin-producing cells are resistant against SDP (Ellermeier *et al.*, 2006).

In order to study the contribution of the BceRS system towards resistance against SDP, we first performed growth measurements of wild type and a mutant carrying unmarked deletions of all three Bce-like systems (Δ*bceRSAB* Δ*psdRSAB* Δ*yxdJKLM-yxeA*) of *B. subtilis* W168 (Gebhard *et al.*, 2014) (TMB1518, referred to as "3x*bce* mutant" hereafter) shown in Fig. 5(a). Although this mutant strain lacks all important peptide antibiotic detoxification modules present in *B. subtilis*, this did not affect growth compared to wild type (Fig. 5a, blue and black curve, respectively). In contrast, comparison of wild type growth to an *sdpI* mutant revealed a severe growth defect upon entry into stationary phase (Fig. 5a, orange curve). Given that the 3x*bce* mutant seems to be unaffected in its growth behavior, we conclude that the BceRS system is not involved in mediating resistance against SDP. Furthermore, we observed no P_{bceA} induction in the 3x*bce* mutant, demonstrating that SDP/SKF cannot be sensed in the absence of the signal transduction system and resistance is not mediated by any of the Bce-like systems (data not shown). This is further supported by the finding that a mutant deficient in both the 3x*bce* resistance modules and the *sdpI* immunity protein (Fig. 5a, pink curve) did not show a stronger growth defect than the *sdpI* mutant alone. To further validate that the BceRS system is indeed not involved in resistance against SDP, we additionally tested the viability of stationary phase cultures (data not shown). We again observed no difference in susceptibility between the 3x*bce sdpI* mutant and the single *sdpI* deletion, underpinning the aforementioned result.

Next, we tested if the BceRS system instead might be involved in mediating resistance against SKF. Towards that end, we deleted *skfEF*, which encode the putative ABC-transporter that is thought to be responsible for export and immunity of SKF and followed growth of a *skfEF* mutant over time (data not shown). In contrast to the *sdpI* deletion, there was no growth defect observable for the *skfEF* mutant. Next, we combined the 3x*bce* mutant with the *skfEF* deletion to see whether the additional 3x*bce* deletion affects growth. But again, the 3x*bce* *skfEF* mutant did not show any growth defect.

Taken together, we found no evidence for a role of Bce-like systems in mediating resistance against SDP and SKF despite its strong induction. We therefore next focused our attention on the specificity of this induction.

Mature SKF toxin strongly acts as inducer

Of the two cannibalism toxins, SKF was the stronger inducer of the *bceA* promoter. Given that the BceRS system did not confer resistance against SKF, we wondered about the physiological relevance of the intrinsic induction of the CESR systems in stationary phase. In order to approach this question, we first had to understand the true nature of the stimulus sensed by the BceRS system. Was it the mature toxin itself or could the unprocessed precursor also lead to its activation? SKF is a ribosomally synthesized AMP and requires posttranslational modification to be fully active (Gonzalez-Pastor *et al.*, 2003; Liu *et al.*, 2010). Our knowledge of this process is still limited and direct evidence for the functions described in the following sentences is still lacking. But it is assumed that the radical SAM (S-adenosyl-methionine) enzyme SkfB mediates the first step in SKF maturation by forming a thioether bond between the cysteine residue Cys4 and the α-carbon of the methionine residue Met12 resulting in pre-SkfA (Flühe *et al.*, 2013; Liu *et al.*, 2010) (Fig. 3). SkfH, a putative thioredoxin oxidoreductase-like protein and the last gene encoded in the *skfA-H* operon is presumed to mediate formation of a disulfide bond leading to SkfA* (Liu *et al.*, 2010) (Fig.

3). Export and immunity was postulated to be mediated by SkfEF, forming an ABC transporter in the membrane (Gonzalez-Pastor *et al.*, 2003). Likewise, SkfC was hypothesized to be responsible for the cyclization reaction prior to or during export of the SKF peptide (Liu *et al.*, 2010). SkfG is so far poorly understood and its function is unknown.

In order to gain deeper insight into the physiological properties of the genes encoded in the *skfA-H* operon, we next studied the intrinsic P_{bceA} induction in different *skf* mutants (Fig. 6a, b). In a *skfA* mutant lacking the structural gene of the SKF toxin, P_{bceA} induction is almost not detectable (Fig. 6b, dark grey curve). Similar results were obtained in a mutant deleted for *skfBC*, the products of which were hypothesized to be involved in maturation of the toxin precursor (Flühe *et al.*, 2013). This suggests that SkfBC perform critical steps in the maturation process of SKF. Likewise, P_{bceA} induction cannot be detected in a *skfEF* mutant, lacking the putative immunity transporter. In contrast, deletion strains lacking either *skfGH* or *skfH* alone were able to activate the BceRS system in stationary phase, albeit 10-fold reduced compared to the wild type reporter strain (see Fig. 1). SkfH is hypothesized to be responsible for one important disulfide bond formation in the maturation process of SKF (Liu *et al.*, 2010). Thus, it seems that SkfH performs a critical step in the maturation of SKF. Additionally, comparison of the *sfkGH* mutant and the *skfBC* or *skfEF* deletion, respectively, revealed that potential modification of SKF by SkfBC and/or export via SkfEF seem to play more crucial roles in the SKF maturation pathway than SkfGH alone, since P_{becA} induction is abolished in both the *skfBC* and *skfEF* mutant. In conclusion, SkfBC and SkfEF are necessary for production of a fully active SKF toxin, while SkfGH seem to play a minor role, at least as judged by the activation of the BceRS system in a *skfGH* mutant.

In order to elucidate if the mature SKF toxin or even its precursor acts as an inducer of the *bceA* promoter, we combined the *sdpC* deletion with the *skfGH* deletion (Fig. 6c, d, orange curve). The resulting double mutant is supposed to be deficient for SDP and lacks crucial steps of SKF maturation. Fig. 6(d) shows that the *sdpC skfGH* double mutant first displayed

significantly decreased BceRS activation, when compared to the *sdpC* deletion mutant (orange vs. grey curve) but after some time (12-13 h), P_{bceA} becomes active although to a much lower extent. This observation might suggest that accumulation of immature SKF precursor could already act as a weak inducer since the time point of induction is much later and the dynamics considerably lower.

Mature SDP toxin acts as inducer

The absence of any role for the BceRS system in mediating resistance against SDP provokes the question why the BceRS system is triggered by this compound. In order to better understand this stimulus leading to P_{bceA} induction, we investigated BceRS activation in individual *sdp* mutants (Fig. 6).

SDP is encoded in the *sdpABC* operon and repressed by AbrB during exponential growth phase and in times of nutrient availability (Chen *et al.*, 2006; Fujita *et al.*, 2005). Upon entry into stationary phase, repression by AbrB is released by active Spo0A, and transcription of the corresponding genes is triggered. Like SKF, SDP is a ribosomally synthesized AMP that requires posttranslational modifications to mature into an active form (Gonzalez-Pastor *et al.*, 2003; Liu *et al.*, 2010; Perez Morales *et al.*, 2013), a process presumably mediated by SdpA and SdpB (Perez Morales *et al.*, 2013). SdpA is thought to be a soluble protein attached to the cytosolic face of the membrane, whereas SdpB is a transmembrane protein (Perez Morales *et al.*, 2013). Together, they are thought to mediate the final step of processing the SDP precursor peptide into active SDP by posttranslational cleavage of the N- and C-terminus (Fig. 3).

To better understand the stimulus leading to P_{bceA} induction by SDP, we first tested if the BceRS system is triggered by the mature SDP toxin or by its precursor. We initially monitored P_{bceA} induction in an *sdpAB* mutant (Fig. 6c, d, blue curve): Compared to the wild type reporter strain (Fig. 1) the induction was only slightly reduced. This is due to the fact that

SKF is still present and acting as the main inducer. Consequently, we next compared P_{bceA} induction in a *skfA-H* mutant and a *skfA-H sdpAB* deletion. As a consequence, a deletion strain of Δ*skfA-H* Δ*sdpAB* would lack SKF and only produce immature, unprocessed SDP precursor that could potentially trigger the BceRS system. Fig. 6(c) and (d) show that the *bceA* promoter induction was completely abolished in the double mutant (green curve), indicating that the SDP precursor is most likely not the inducer of the *bceA* promoter, but rather the mature SDP.

Next, we tested *bceA* promoter induction in an *sdpI* mutant, lacking the autoimmunity against SDP (Fig. 5b, c). Surprisingly, P_{bceA} induction was completely abolished in this strain. This unexpected finding provoked the question if the *sdp*/*skf* operons are still expressed in an *sdpI* mutant since a loss of auto-immunity has previously been reported to sometimes abolish toxin production (Foulston & Bibb, 2010). Both P_{sdpA} and P_{skfA} showed a strong increase about 10-fold and 100-fold, respectively (Fig. 5c, green and blue curve, respectively), comparable to wild type results (see Fig. 4), demonstrating that the two toxin promoters are fully induced and the toxins are most likely also produced. Because of the severe growth defects of the *sdpI* mutant, we wondered whether the silence in the BceRS system is maybe a result of this growth defect. However, addition of bacitracin (10 μg ml^{-1}) to stationary phase cultures could still fully activate the BceRS system (Fig. 5c), demonstrating that the BceRS system itself is still functional in the *sdpI* mutant.

We next addressed the question if SDP itself is still produced as a potent toxin in the *sdpI* mutant. To this end, we performed a spot-on-lawn assay using a *spo0A* deletion strain as sensitive lawn (Fig. 5d). Since cannibalism toxin production and immunity is regulated in a Spo0A-dependent manner, a *spo0A* mutant is unable to produce both SDP and SKF and is therefore sensitive against both toxins. We spotted stationary phase cultures of wild type as well as *sdp* and *skf* mutants on a plate containing Δ*spo0A* lawn cells and compared zones of inhibition after incubation overnight. Wild type spots showed a clear zone of inhibition on the

spo0A lawn indicating production of functional cannibalism toxins. We then used a *skfA* deletion strain lacking SKF toxin but still expressing SDP. We found that the *skfA* mutant showed a clear inhibition zone just like wild type, indicating production of functional SDP toxin in the absence of SKF. Accordingly, we took an *sdpC* deletion strain lacking SDP but still producing SKF. However, Δ*sdpC* was unable to kill *spo0A* deficient cells, demonstrating that SDP rather than SKF is the major cannibalism toxin on solid medium, which is in agreement with a previous study (Liu *et al.*, 2010). Importantly, a significant zone of inhibition comparable in size to the wild type can be observed around spots of an *sdpI* deletion mutant. This result unequivocally demonstrates that functional SDP toxin is still produced in an *sdpI* mutant. Nevertheless, BceRS activation was abolished in this strain. This observation indicates a link between toxin sensing by the BceRS system and the presence of the immunity protein SdpI. While understanding the molecular mechanism behind this finding is beyond the scope of this work and will require further investigations, it already points towards an indirect way of sensing as will be discussed below. **[3074 words]**

Conclusion

Our results demonstrate that the BceRS system is intrinsically activated in late-stationary phase due to the production of two cannibalism toxins, SDP and SKF, with SKF being the stronger inducer. The *skfA-H* deletion resulted in a 100-fold reduced BceRS activity, whereas the *sdpC* deletion caused only a 10-fold reduced P_{bceA} induction (Fig. 2b). The exact physiological role of the BceRS system in the cannibalism stress response, however, remains unclear. Our data suggests that it provides no role in resistance against either SDP or SKF. However, it seems that the immunity determinants SdpI and SkfEF, respectively, are important for triggering the BceRS response since in corresponding deletion strains BceRS activation is abolished (Figs 5+6). For SkfEF, this finding is less surprising since this ABC-transporter is thought to also export the SKF toxin. Hence, in its absence no mature inducer reaches the extracellular environment to trigger a BceRS response. But at present, this assumption is hard to investigate without a detectable SKF-dependent phenotype.

SDP was shown to be the weaker inducer of the *bceA* promorter, displaying only a 10-fold reduced BceRS response in an *sdpC* mutant compared to the wild type (Fig. 2). Remarkably, in an *sdpI* deletion, we observed a complete loss of the BceRS response despite the fact that both toxin loci are fully expressed (Figs 4b+5c) and SDP is most likely functionally produced (Fig. 5d).

Taken together, these findings indicate that SdpI is required for SDP and potentially also SKF perception by the BceRS system (Fig. 7). This mode of an indirect sensing of SDP only in complex with SdpI resembles the mode for bacitracin perception for the BceRS system that was suggested recently (Kingston *et al.*, 2014). Here, it has been proposed that only the complex of bacitracin to its membrane target, undecaprenol pyrophosphate, can act as a trigger of the BceRS response. Our findings on an SdpI-dependent sensing of SDP (and potentially also SKF) support this model of AMP perception by the BceRS system, in which

401 the toxin/AMP has to be bound to a membrane target before it can be perceived by the BceRS
402 system. Analyzing this novel mechanism will be the subject of further investigations.
403 Nevertheless, our results provide clear evidence for a tight link between signaling systems
404 that mediate the CESR in *B. subtilis* and intrinsic AMP production as part of the stationary
405 phase survival strategy of this organism. **[394 words]**
406

407 **Acknowledgements**
408 This project was funded by the DFG priority program SPP1617 "Phenotypic Heterogeneity
409 and Sociobiology of Bacterial Populations" (grant MA 2837/3-1 to TM). **[22 words]**

410 **Table 1:** Strains used in this study.

411

***E. coli* strain**	**Genotype**	**Reference**
DH5α	*recA1 endA1 gyrA96 thi hsdR17*rK- mK+*relA1 supE44 ϕ*80Δ*lacZ*Δ*M15* Δ(*lacZYA-argF*)*U169*	(Sambrook & Russell, 2001)
XL1-blue	*endA1 gyrA96*(*nal*^{R}) *thi*-1 *recA1 relA1 lac gln*V44 F′[Tn10 *proAB*$^{+}$ *lacI*^{q} Δ(*lacZ*)*M15*] *hsdR17*(rK^{-} mK^{+}) *tet*^{R}	lab stock
***B. subtilis* strain**	**Genotype**	**Reference**
W168	*trpC2*	lab stock
TMB1518	W168 Δ*bceRSAB psdRSAB yxdJKLM yxeA* (clean)	(Gebhard *et al.*, 2014)
TMB1528	W168 *sdpI*::mls	this study
TMB1578	W168 *sacA*::*luxABCDE* (without promoter)	this study
TMB1619	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*)	this study
TMB1620	W168 *sacA*::pCHlux104 (P_{bcrC}-*lux*)	this study
TMB1768	W168 *sdpC*::kan	this study
TMB1770	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *sdpC*::kan	this study
TMB1773	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *skfA-H*::spec	this study
TMB1775	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *yydF-J*::spec	this study
TMB1843	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *sunA*::kan	this study
TMB1985	W168 *sacA*::pJHlux102 (P_{sdpA}-*lux*)	this study
TMB2009	W168 *sacA*::pJHlux104 (P_{psdA}-*lux*)	this study
TMB2015	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *sdpC*::kan *skfA-H*::spec	this study
TMB2016	W168 *sacA*::pJHlux105 (P_{skfA}-*lux*)	this study
TMB2047	W168 *sacA*::pJHlux104 (P_{psdA}-*lux*) *sdpC*::kan	this study
TMB2048	W168 *sacA*::pJHlux104 (P_{psdA}-*lux*) *skfA-H*::spec	this study
TMB2118	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *sdpI*::mls	this study
TMB2164	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *skfA-H*::spec *sdpAB*::mls	this study
TMB2166	W168 Δ*bceRSAB psdRSAB yxdJKLM yxeA* (clean) *sdpI*::mls	this study
TMB2207	W168 *sacA*::pCHlux104 (P_{bcrC}-*lux*) *sdpC*::kan	this study
TMB2208	W168 *sacA*::pCHlux104 (P_{bcrC}-*lux*) *skfA-H*::spec	this study
TMB2209	W168 *sacA*::pCHlux104 (P_{bcrC}-*lux*) *sunA*::kan	this study
TMB2210	W168 *sacA*::pCHlux104 (P_{bcrC}-*lux*) *yydF-J*::spec	this study
TMB2211	W168 *sacA*::pJHlux102 (P_{sdpA}-*lux*) *sdpI*::mls	this study
TMB2212	W168 *sacA*::pJHlux105 (P_{skfA}-*lux*) *sdpI*::mls	this study
TMB2221	W168 *sacA*::pCHlux104 (P_{bcrC}-*lux*) *sdpC*::kan *skfA-H*::spec	this study
TMB2222	W168 *sacA*::pJHlux104 (P_{psdA}-*lux*) *sdpC*::kan *skfA-H*::spec	this study
TMB2223	W168 *sacA*::pJHlux104 (P_{psdA}-*lux*) *yydF-J*::spec	this study
TMB2224	W168 *sacA*::pJHlux104 (P_{psdA}-*lux*) *sunA*::kan	this study
TMB2240	W168 *spo0A*::spec	this study
TMB2257	W168 *sacA*::pCH3Clux02 (P_{sigX}-*lux*)	this study
TMB2259	W168 *sacA*::pCH3Clux04 (P_{ydaH}-*lux*)	this study
TMB2260	W168 *skfA*::mls	this study
TMB2262	W168 *skfEF*::mls	this study
TMB2265	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *skfA*::mls	this study
TMB2266	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *skfBC*::spec	this study
TMB2267	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *skfEF*::mls	this study

TMB2268	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *skfH*::kan	this study
TMB2299	W168 *sacA*::pASp3Clux01 (P_{pspA}-*lux*)	this study
TMB2339	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *skfGH*::kan	this study
TMB2806	W168 *sacA*::pCHlux103 (P_{bceA}-*lux*) *sdpC*::kan *skfGH*::mls	this study
TMB2909	W168 Δ*bceRSAB psdRSAB yxdJKLM yxeA* (clean) *skfEF*::mls	this study

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413

414 **Table 2:** Vectors and plasmids used in this study

415

Plasmid/vector	Genotype[a]	Primers used for cloning	Reference or source
pAH328	*sacA*'…'*sacA*, *luxABCDE*, *bla*, *cat*		(Schmalisch *et al.*, 2010)
pBS3Clux	pAH328 derivative; *sacA*'…'*sacA*, *luxABCDE*, *bla*, *cat*		(Radeck *et al.*, 2013)
pCHlux103	pAH328 derivative, *sacA*::P_{bceA}-*lux*, *cat*	TM2513/2514	This study
pCHlux104	pAH328 derivative, *sacA*::P_{bcrC}-*lux*, *cat*	TM2515/2516	This study
pJHlux102	pAH328 derivative, *sacA*::P_{sdpA}-*lux*, *cat*	TM2785/2786	This study
pJHlux104	pAH328 derivative, *sacA*::P_{psdA}-*lux*, *cat*	TM2781/2782	This study
pJHlux105	pAH328 derivative, *sacA*::P_{skfA}-*lux*, *cat*	TM2783/2784	This study
pCH3Clux02	pAH328 derivative, *sacA*::P_{sigX}-*lux*, *cat*	TM3262/3263	This study
pCH3Clux04	pAH328 derivative, *sacA*::P_{ydaH}-*lux*, *cat*	TM3266/3267	This study
pASp3Clux01	pAH328 derivative, *sacA*::P_{pspA}-*lux*, *cat*	TM3268/3269	This study

416 [a]Resistance cassettes: bla = ampicillin, cat = chloramphenicol

417

418 **Table 3:** Oligonucleotides used in this study.

419

Primer name	Sequence 5' – 3'[a]
Construction of transcriptional promoter-lux fusions	
TM2513 P_{bceA} *Not*I fwd	a***gcggccgc***ACGCGGTGAAATACAGCGAAG
TM2514 P_{bceA} *Sal*I rev	taa***gtcgac***TATATTGGATAATCTCATTATAAAAAG
TM2515 P_{bcrC} *Not*I fwd	a***gcggccgc***GGCCTTCAAAAAGCACATACG
TM2516 P_{bcrC} *Sal*I rev	taa***gtcgac***TTACATTTTTATATTTAGTAGACTAATC
TM2785 P_{sdpA} *EcoR*I fwd	ttatag***gaattc***cgcggccgcttctagagGATGACGCTTACGGAATTATCTG
TM2786 P_{sdpA} *Spe*I rev	ctataa***actagt***TTTTTTGATGTAGATTACCTCCTC
TM2781 P_{psdA} *EcoR*I fwd	ttatag***gaattc***cgcggccgcttctagagTGATGCTGCAAACGGCCC
TM2782 P_{psdA} *Spe*I rev	ctataa***actagt***TTTCTTTATTATAAAAAGGAAGTCAGC
TM2783 P_{skfA} *EcoR*I fwd	ttatag***gaattc***cgcggccgcttctagagATGACAGATTCGTATTGCCGG
TM2784 P_{skfA} *Spe*I rev	ctataa***actagt***TCAATTTTTGCATAGAGTCTATTGAC
TM3262 P_{sigX} *EcoR*I fwd	ttatag***gaattc***cgcggccgcttctagagACTCCGGGTCTGGCATACC
TM3263 P_{sigX} *Spe*I rev	ctataa***actagt***TCACTTTTTTGTCGTATGAATAGCTTG
TM3266 P_{ydaH} *EcoR*I fwd	ttatag***gaattc***cgcggccgcttctagagTTTGAGAGAGAAGCTTACCGC
TM3267 P_{ydaH} *Spe*I rev	ctataa***actagt***AATTTCATCCTAGAGATAAGACTGG
TM3268 P_{pspA} *EcoR*I fwd	ttatag***gaattc***cgcggccgcttctagagTCCGGTGACATCAATTGACTC
TM3269 P_{pspA} *Spe*I rev	ctataa***actagt***AAAGCTAATTCGGTAACCCTTG
Allelic replacement mutagenesis (LFH-PCR)	
TM2748 *sdpC* up fwd	GAAGGTTATATTGACACCTATAATCC
TM2749 *sdpC* up rev	*CCTATCACCTCAAATGGTTCGCTG*GTTACCATGGAAACAATCAATAGCC
TM2750 *sdpC* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*GCTGCTGCAAAAACCCTAAAATTG
TM2751 *sdpC* do rev	CAAATATCTAAATGTCTAAATGTTTTTTTGTAAAG
TM2744 *skf* up fwd	TGGTGCGTTAGGGGTTATGATTGC
TM2745 *skf* up rev	*CCTATCACCTCAAATGGTTCGCTG*CTCACAGATTCCCATTCTTTTTGG
TM2746 *skf* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*GGAGATGTTGGTTGGGATAAGATG

TM2747 *skf* do rev	GATTTGCTGCCGTTTTGGTAAGAC
TM2723 *sunA* up fwd	GTATCACGATGGATATTTATAGATGC
TM2724 *sunA* up rev	*CCTATCACCTCAAATGGTTCGCTG*GTTTTCGAGTTCCTCTAGTTTAACTTC
TM2725 *sunA* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*GAGCTGTTGCTTGTCAAAACTATC
TM2726 *sunA* do rev	GGGAGAATAATTGTTAAGAAAAGAATG
TM3138 *sdpAB* up fwd	CAGACAATTGAATGCTTCCC
TM3139 *sdpAB* up rev	*CCTATCACCTCAAATGGTTCGCTG*GCTAAAGTAATAAGAAGAAAATAATAG
TM3140 *sdpAB* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*GGTGAATCAGTCAAGTTTCTTAC
TM3141 *sdpAB* do rev	GTGGAAATTCTATGCAGCTAG
TM0307 *spo0A* up fwd	TATCAGAGATTCTGCTGCTGGC
TM0308 *spo0A* up rev	*CCTATCACCTCAAATGGTTCGCTG*AGCGACAGGCATTCCTGTCC
TM0309 *spo0A* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*GTTGCGGATAAGCTGAGG
TM0310 *spo0A* do rev	GGAAGAACCTGAGACACCG
TM3315 *skfA* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*CGTGTTTGTGCACTTCCGCATC
TM3316 *skfA* do rev	GCTTCCCTAAGCTGTATTTGAACC
TM3317 *skfBC* up fwd	GTACAGTACGATTGCCTTGATCG
TM3318 *skfBC* up rev	*CCTATCACCTCAAATGGTTCGCTG*GAACCGCTAACTCTGGCAAATC
TM3319 *skfBC* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*GAAACATATGCATCATGATCAGCC
TM3320 *skfBC* do rev	CTGCCATTTGACTTGGTAATCG
TM3321 *skfEF* up fwd	CAGTACTTATTGGTACATAGCGG
TM3322 *skfEF* up rev	*CCTATCACCTCAAATGGTTCGCTG*CATCACCATTTCGATAGCATTTGC
TM3323 *skfEF* do fwd	*CGAGCGCCTACGAGGAATTTGTATCG*CATAGGGAGCCTAAGTTGGTG
TM3324 *skfEF* do rev	CATCGTTTTAGTAATGATCTGACC
TM3325 *skfH* up fwd	GAATTGTCAGACATTCTCAATCAG
TM3326 *skfH* up rev	*CCTATCACCTCAAATGGTTCGCTG*CTTGGCCATTCAGTCAACATTTG
TM3393 *skfGH* up fwd	GTGCCAGAACAGTGAAGAAAATG
TM3394 *skfGH* up rev	*CCTATCACCTCAAATGTTCGCTG*GAACAGATAACGACAATTTATCACC

TM0137 kan fwd	CAGCGAACCATTTGAGGTGATAGG
TM0138 kan rev	CGATACAAATTCCTCGTAGGCGCTCGG
TM0139 mls fwd	CAGCGAACCATTTGAGGTGATAGGGATCCTTTAACTCTGGCAACCCTC
TM0140 mls rev	CGATACAAATTCCTCGTAGGCGCTCGGGCCGACTGCGCAAAAGACATAATCG
TM0141 spec fwd	CAGCGAACCATTTGAGGTGATAGGGACTGGCTCGCTAATAACGTAACGTGACTGGCAAGAG
TM0142 spec rev	CGATACAAATTCCTCGTAGGCGCTCGGCGTAGCGAGGGCAAGGGTTTATTGTTTTCTAAAATCTG
Check primers	
TM2505 *sacA* front check fwd	CTGATTGGCATGGCGATTGC
TM2506 *sacA* front check rev	ACAGCTCCAGATCCTCTACG
TM2507 *sacA* back check fwd	GTCGCTACCATTACCAGTTG
TM2508 *sacA* back check rev	TCCAAACATTCCGGTGTTATC
TM2262 pAH328 check fwd	GAGCGTAGCGAAAAATCC
TM2263 pAH328 check rev	GAAATGATGCTCCAGTAACC

[a]Restriction sites are highlighted in bold italics; BioBrick overhang sequences are underlined; overhang sequences for resistance cassettes are marked in italics.

Figure legends

Figure 1: Intrinsic late-stationary phase induction of P_{bceA}-*lux*, P_{psdA}-*lux* (a, b) and ECF σ factor target promoters in W168 (c, d).

Promoter activity was detected by following luminescence of 100 µl cultures growing in a microplate reader (Biotek®, Synergy™2; 96-well plate, 37°C, shaking) over time. The upper graphs (a, c) show the growth curves (OD_{600}) of the respective strains in MCSE medium. The lower graphs (b, d) show the promoter activities as relative luminescence units (RLU) per OD_{600}. Late-stationary phase induction is shown for both the P_{bceA} (black) and P_{psdA} (orange) after 7-8 h of growth (b). Induction of P_{bcrC} controlled by σ^M, σ^X and σ^W after 7-8 h of growth is shown in green (d). Intermediate induction of σ^X- and σ^M-dependent promoters (P_{sigX} and P_{ydaH}) is shown in red and purple, respectively, after 7-8 h of growth. The σ^W-dependent P_{pspA} (blue) stays uninduced under our cultivation conditions. Please note that the small peak at t=5 in this and all the following figures does not represent a regulated transition phase promoter induction, since it was observed for any promoter studied in MCSE so far, including a set of known constitutive promoters (Radeck *et al.*, 2013). All graphs show mean values and SEM (standard error of the mean) of at least three independent replicates.

Figure 2: Late-stationary phase induction of P_{bceA}-*lux* (a, b), P_{psdA}-*lux* (c, d) and P_{bcrC}-*lux* (e, f) in deletion backgrounds.

Promoter activity was detected by following luminescence in a microplate reader (for details see legend Fig. 1). Panels (b), (d) and (f) show the effect of different strains deleted for various antimicrobial peptide loci on each promoter: Δ*sunA* (Sublancin) in light brown, Δ*yydF-J* (YydF peptide) in dark purple, Δ*sdpC* (SDP) in blue, Δ*skfA-H* (SKF) in green, Δ*sdpC*Δ*skfA-H* in red. Δ*sunA* had no effect on either promoter. Δ*yydF-J* showed only minor effects on P_{bceA}, P_{psdA} and P_{bcrC} activity in stationary phase. Deletion of *sdpC* revealed 10-fold decrease on P_{bceA} activity and approx. 7-fold on P_{psdA} and P_{bcrC} activity. The *skfA-H* deletion resulted in approx. 100-fold reduced P_{bceA} and P_{psdA} activity but only 4-fold reduced P_{bcrC} induction.

Figure 3: Schematic overview of SDP and SKF maturation and genomic context.

Panels (a) and (c) show main transcripts of the *sdpABC-sdpRI* and *skfA-H* operons, each based on recent microarray studies (Nicolas *et al.*, 2012). Panels (b) and (d) show the hypothesized schematic maturation pathway of SDP and SKF precursors until release of the final toxin. According to Perez Morales *et al.*, 2013 pro-SdpC is translocated across the membrane by the

general secretory pathway (Sec) and the leader peptide thereby cleaved by the SipS/T peptidase (b). SdpAB further cleave SdpC* at the N-and C-termini to release the final SDP toxin to the environment. Similarly, pro-SkfA is hypothesized to be modified by SkfB to give pre-SkfA which is assumed to be further processed by SkfH to prepare for export and cyclization by SkfEF and SkfC, respectively (d). These assumptions are based on Liu *et al.*, 2010 and lack further evidence.

Figure 4: Correlation of P_{sdpA} and P_{skfA} activities with P_{bceA} induction.

Promoter activity was detected by following luminescence in a microplate reader (for details see legend Fig. 1). P_{sdpA} and P_{skfA} activity is shown over time (in green and blue, respectively). P_{bceA} induction is shown for comparison (black). P_{sdpA} revealed a higher basal activity compared to P_{skfA} and showed approx. 10-fold induction in stationary phase starting around 5 h after beginning of the experiment. P_{skfA} exhibited a similar induction pattern starting slightly later (5-6 h) showing approx. 100-fold induction.

Figure 5: Effect of an *sdpI* and a triple *bceRSAB psdRSAB yxdJKML-yxeA* mutant on SDP sensitivity.

(a) Growth in W168 (black) and Δ*bceRSAB* Δ*psdRSAB* Δ*yxdJKLM-yxeA* (referred to as Δ3x*bce* hereafter, blue) was similar whereas growth in Δ*sdpI* (orange) was impaired starting after entry into stationary phase. However, growth was not further impaired in Δ3x*bce* Δ*sdpI* (pink) indicating no additional role of the BceRS system in resistance against SDP. P_{bceA}, P_{sdpA} and P_{skfA} growth and induction (b, c) were detected by following luminescence in a plate reader (for details see legend Fig. 1). P_{bceA} is not intrinsically induced in Δ*sdpI* (black filled circles) whereas P_{sdpA} and P_{skfA} are activated after 5-6 h upon start of the experiment (green and blue, respectively) indicating correct expression of the respective loci. Upon induction with bacitracin (10 µg ml^{-1}) at t=9 h, P_{bceA} is fully activated (black open circles). Negative data points and values smaller than 50 RLU/OD_{600} are not depicted. Error bars smaller than symbols are not shown. In panel (d), stationary phase cells of W168 and mutants were applied to a plate containing a lawn of Δ*spo0A* cells. From left to right: W168, Δ*skfA* (SKF), Δ*sdpC* (SDP) and Δ*sdpI* (immunity protein against SDP). Halo indicates production of mature SDP. An *sdpC* mutant strain is unable to kill *spo0A* deficient cells. SDP seems to be the major cannibalism toxin on solid medium.

Figure 6: P_{bceA} activity in different *sdp* and *skf* mutants.

Promoter activity was detected by following luminescence in a microplate reader (for details see legend Fig. 1). P_{bceA} activity in Δ*skfA* (dark grey), Δ*skfBC* (middle grey) and Δ*skfEF* (light grey) is abolished (b). P_{bceA} response in Δ*skfGH* (orange) and Δ*skfH* (red) is about 10-fold reduced (b) compared to W168 (see Fig. 1). The time delay of promoter induction in Δ*skfGH* (orange) is due to an approx. 2 h prolonged lag phase but stays the same regarding stationary phase induction point. P_{bceA} induction in Δ*sdpAB*Δ*skfA-H* (d, green curve) as well as Δ*sdpC*Δ*skfGH* (d, orange curve) is lost indicating that posttranslational modification of SDP and SKF by SdpAB and SkfGH, each, is needed to activate the BceRS system.

Figure 7: Model of SDP/SKF sensing by the BceRS system.

SdpI binding to SDP (and maybe SKF) is a prerequisite for sensing by the BceRS system. The BceRS system consists of an ABC-transporter, BceAB (short A, B) responsible for the detection of bacitracin (Bac) and is coupled to a TCS consisting of a histidine kinase BceS (short: S) and its cognate response regulator, BceR (short: R). Detection of Bac leads to an induction of P_{bceA} and subsequent transcription of AB to mediate resistance. Current research argues about Bac recognition by AB. One hypothesis is that it has to bind its target UPP (undecaprenol pyrophosphate) in the bacterial membrane in order to be sensed by AB. Taken this hypothesis for granted it could be that only the SdpI-SDP complex can be recognized by AB. ECF σ^W is induced by SDP (and SKF?) and provides a second layer of resistance.

References

Albano, M., Smits, W. K., Ho, L. T., Kraigher, B., Mandic-Mulec, I., Kuipers, O. P. & Dubnau, D. (2005). The Rok protein of *Bacillus subtilis* represses genes for cell surface and extracellular functions. *J Bacteriol* **187**, 2010-2019.

Breukink, E. & de Kruijff, B. (2006). Lipid II as a target for antibiotics. *Nat Rev Drug Discov* **5**, 321-332.

Butcher, B. G. & Helmann, J. D. (2006). Identification of *Bacillus subtilis* σ^{W}-dependent genes that provide intrinsic resistance to antimicrobial compounds produced by Bacilli. *Mol Microbiol* **60**, 765-782.

Butcher, B. G., Lin, Y.-P. & Helmann, J. D. (2007). The *yydFGHIJ* operon of *Bacillus subtilis* encodes a peptide that induces the LiaRS two-component system. *J Bacteriol* **189**, 8616-8625.

Chen, G., Kumar, A., Wyman, T. H. & Moran, C. P., Jr. (2006). Spo0A-dependent activation of an extended -10 region promoter in *Bacillus subtilis*. *J Bacteriol* **188**, 1411-1418.

Chung, J. D., Stephanopoulos, G., Ireton, K. & Grossman, A. D. (1994). Gene expression in single cells of *Bacillus subtilis*: evidence that a threshold mechanism controls the initiation of sporulation. *J Bacteriol* **176**, 1977-1984.

Cutting, S. M. & Van der Horn, P. B. (1990). Genetic analysis. In Molecular Biological Methods for *Bacillus*, pp. 27-74. Edited by C. R. Harwood & S. M. Cutting. Chichester, United Kingdom: John Wiley & Sons, Ltd.

Dominguez-Escobar, J., Wolf, D., Fritz, G., Höfler, C., Wedlich-Söldner, R. & Mascher, T. (2014). Subcellular localization, interactions and dynamics of the phage-shock protein-like Lia response in *Bacillus subtilis*. *Mol Microbiol* **92**, 716-732.

Dubois, J. Y., Kouwen, T. R., Schurich, A. K., Reis, C. R., Ensing, H. T., Trip, E. N., Zweers, J. C. & van Dijl, J. M. (2009). Immunity to the bacteriocin sublancin 168 Is determined by the SunI (YolF) protein of *Bacillus subtilis*. *Antimicrobial agents and chemotherapy* **53**, 651-661.

Ellermeier, C. D., Hobbs, E. C., Gonzalez-Pastor, J. E. & Losick, R. (2006). A three-protein signaling pathway governing immunity to a bacterial cannibalism toxin. *Cell* **124**, 549-559.

Flühe, L., Burghaus, O., Wieckowski, B. M., Giessen, T. W., Linne, U. & Marahiel, M. A. (2013). Two [4Fe-4S] clusters containing radical SAM enzyme SkfB catalyze thioether

bond formation during the maturation of the sporulation killing factor. *Journal of the American Chemical Society* **135**, 959-962.

Foulston, L. C. & Bibb, M. J. (2010). Microbisporicin gene cluster reveals unusual features of lantibiotic biosynthesis in actinomycetes. *Proc Natl Acad Sci U S A* **107**, 13461-13466.

Fujita, M., Gonzalez-Pastor, J. E. & Losick, R. (2005). High- and low-threshold genes in the Spo0A regulon of *Bacillus subtilis*. *J Bacteriol* **187**, 1357-1368.

Gebhard, S., Fang, C., Shaaly, A., Leslie, D. J., Weimar, M. R., Kalamorz, F., Carne, A. & Cook, G. M. (2014). Identification and characterization of a bacitracin resistance network in *Enterococcus faecalis*. *Antimicrobial agents and chemotherapy* **58**, 1425-1433.

Gonzalez-Pastor, J. E., Hobbs, E. C. & Losick, R. (2003). Cannibalism by sporulating bacteria. *Science* **301**, 510-513.

Harwood, C. R. & Cutting, S. M. (1990). Molecular Biological Methods for *Bacillus*. Chichester: John Wiley & Sons.

Helmann, J. D. (2002). The extracytoplasmic function (ECF) sigma factors. *Adv Microb Physiol* **46**, 47-110.

Huang, X., Fredrick, K. L. & Helmann, J. D. (1998). Promoter recognition by *Bacillus subtilis* σ^W: autoregulation and partial overlap with the σ^X regulon. *J Bacteriol* **180**, 3765-3770.

Jordan, S., Rietkötter, E., Strauch, M. A., Kalamorz, F., Butcher, B. G., Helmann, J. D. & Mascher, T. (2007). LiaRS-dependent gene expression is embedded in transition state regulation in *Bacillus subtilis*. *Microbiology* **153**, 2530-2540.

Kallenberg, F., Dintner, S., Schmitz, R. & Gebhard, S. (2013). Identification of regions important for resistance and signalling within the antimicrobial peptide transporter BceAB of *Bacillus subtilis*. *J Bacteriol* **195**, 3287-3297.

Kingston, A. W., Liao, X. & Helmann, J. D. (2013). Contributions of the σ^W , σ^M and σ^X regulons to the lantibiotic resistome of *Bacillus subtilis*. *Mol Microbiol* **90**, 502-518.

Kingston, A. W., Zhao, H., Cook, G. M. & Helmann, J. D. (2014). Accumulation of heptaprenyl diphosphate sensitizes Bacillus subtilis to bacitracin: implications for the mechanism of resistance mediated by the BceAB transporter. *Mol Microbiol* **93**, 37-49.

Liu, W. T., Yang, Y. L., Xu, Y., Lamsa, A., Haste, N. M., Yang, J. Y., Ng, J., Gonzalez, D., Ellermeier, C. D. & other authors (2010). Imaging mass spectrometry of intraspecies

metabolic exchange revealed the cannibalistic factors of *Bacillus subtilis*. *Proc Natl Acad Sci U S A* **107**, 16286-16290.

Mascher, T., Margulis, N. G., Wang, T., Ye, R. W. & Helmann, J. D. (2003). Cell wall stress responses in *Bacillus subtilis*: the regulatory network of the bacitracin stimulon. *Mol Microbiol* **50**, 1591-1604.

Mascher, T., Hachmann, A. B. & Helmann, J. D. (2007). Regulatory overlap and functional redundancy among *Bacillus subtilis* extracytoplasmic function (ECF) σ factors. *J Bacteriol* **189**, 6919-6927.

Missiakas, D. & Raina, S. (1998). The extracytoplasmic function sigma factors: role and regulation. *Mol Microbiol* **28**, 1059-1066.

Nakano, M. M., Zheng, G. & Zuber, P. (2000). Dual control of *sbo-alb* operon expression by the Spo0 and ResDE systems of signal transduction under anaerobic conditions in *Bacillus subtilis*. *J Bacteriol* **182**, 3274-3277.

Nicolas, P., Mäder, U., Dervyn, E., Rochat, T., Leduc, A., Pigeonneau, N., Bidnenko, E., Marchadier, E., Hoebeke, M. & other authors (2012). Condition-dependent transcriptome reveals high-level regulatory architecture in *Bacillus subtilis*. *Science* **335**, 1103-1106.

Oman, T. J., Boettcher, J. M., Wang, H., Okalibe, X. N. & van der Donk, W. A. (2011). Sublancin is not a lantibiotic but an S-linked glycopeptide. *Nature chemical biology* **7**, 78-80.

Perez Morales, T. G., Ho, T. D., Liu, W. T., Dorrestein, P. C. & Ellermeier, C. D. (2013). Production of the cannibalism toxin SDP is a multistep process that requires SdpA and SdpB. *J Bacteriol* **195**, 3244-3251.

Radeck, J., Kraft, K., Bartels, J., Cikovic, T., Dürr, F., Emenegger, J., Kelterborn, S., Sauer, C., Fritz, G. & other authors (2013). The *Bacillus* BioBrick Box: generation and evaluation of essential genetic building blocks for standardized work with *Bacillus subtilis*. *J Biol Eng* **7**, 29.

Rietkötter, E., Hoyer, D. & Mascher, T. (2008). Bacitracin sensing in *Bacillus subtilis*. *Mol Microbiol* **68**, 768-785.

Sambrook, J. & Russell, D. W. (2001). Molecular Cloning - a laboratory manual. Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory Press.

Schmalisch, M., Maiques, E., Nikolov, L., Camp, A. H., Chevreux, B., Muffler, A., Rodriguez, S., Perkins, J. & Losick, R. (2010). Small genes under sporulation control in the *Bacillus subtilis* genome. *J Bacteriol* **192**, 5402-5412.

Schrecke, K., Staroń, A. & Mascher, T. (2012). Two-component signaling in the Gram-positive envelope stress response: intramembrane-sensing histidine kinases and accessory membrane proteins. In Two component systems in bacteria, pp. 199-229. Edited by R. Gross & D. Beier. Hethersett, Norwich, UK: Horizon Scientific Press.

Silver, L. L. (2003). Novel inhibitors of bacterial cell wall synthesis. *Current opinion in microbiology* **6**, 431-438.

Silver, L. L. (2006). Does the cell wall of bacteria remain a viable source of targets for novel antibiotics? *Biochem Pharmacol* **71**, 996-1005.

Staroń, A., Finkeisen, D. E. & Mascher, T. (2011). Peptide antibiotic sensing and detoxification modules of *Bacillus subtilis*. *Antimicrobial agents and chemotherapy* **55**, 515-525.

Strauch, M. A., Bobay, B. G., Cavanagh, J., Yao, F., Wilson, A. & Le Breton, Y. (2007). Abh and AbrB control of *Bacillus subtilis* antimicrobial gene expression. *J Bacteriol* **189**, 7720-7732.

Walsh, C. (2003). Antibiotics - actions, origins, resistance. Washington, D.C.: ASM press.

Wolf, D., Kalamorz, F., Wecke, T., Juszczak, A., Mäder, U., Homuth, G., Jordan, S., Kirstein, J., Hoppert, M. & other authors (2010). In-depth profiling of the LiaR response of *Bacillus subtilis*. *J Bacteriol* **192**, 4680-4693.

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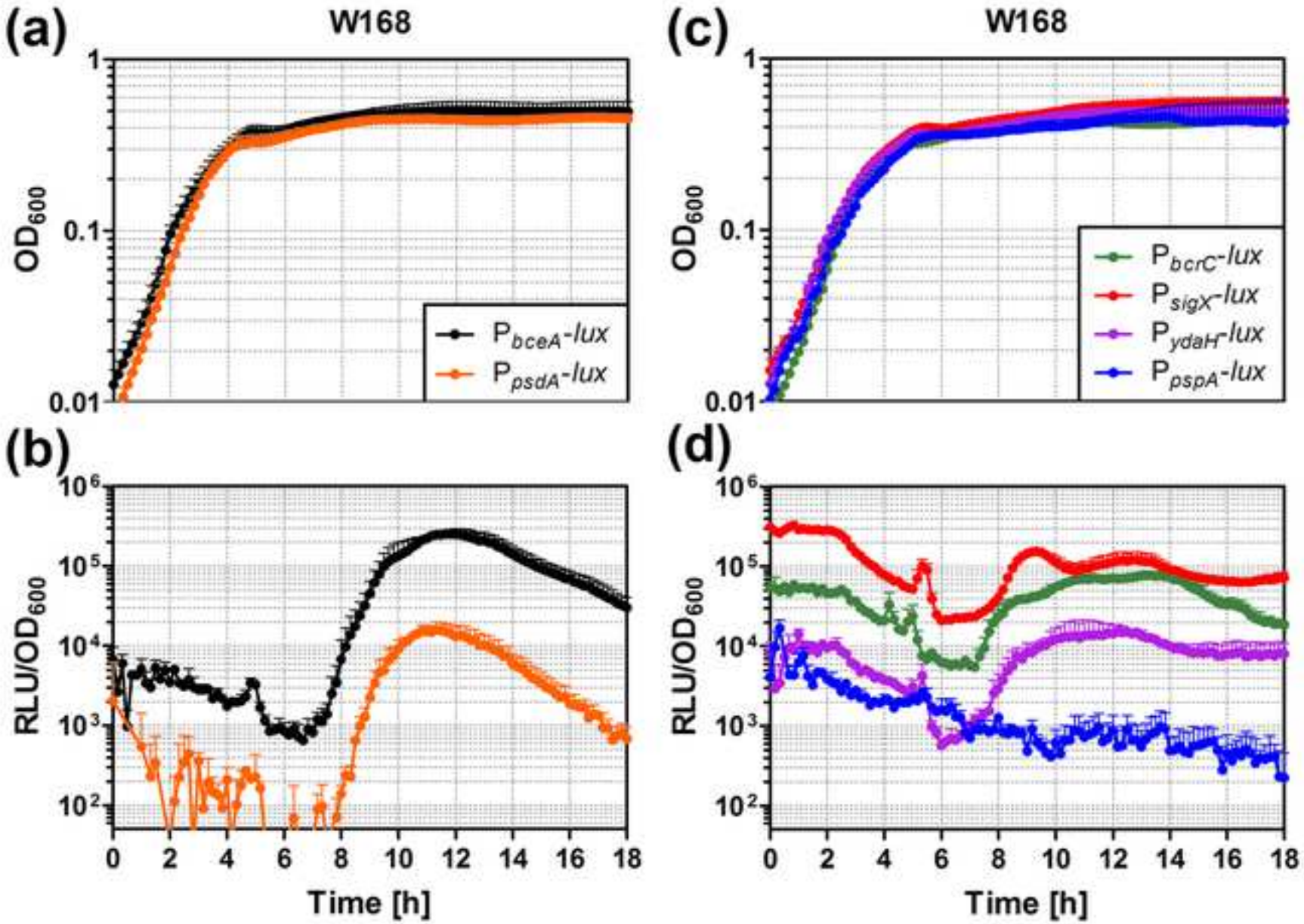

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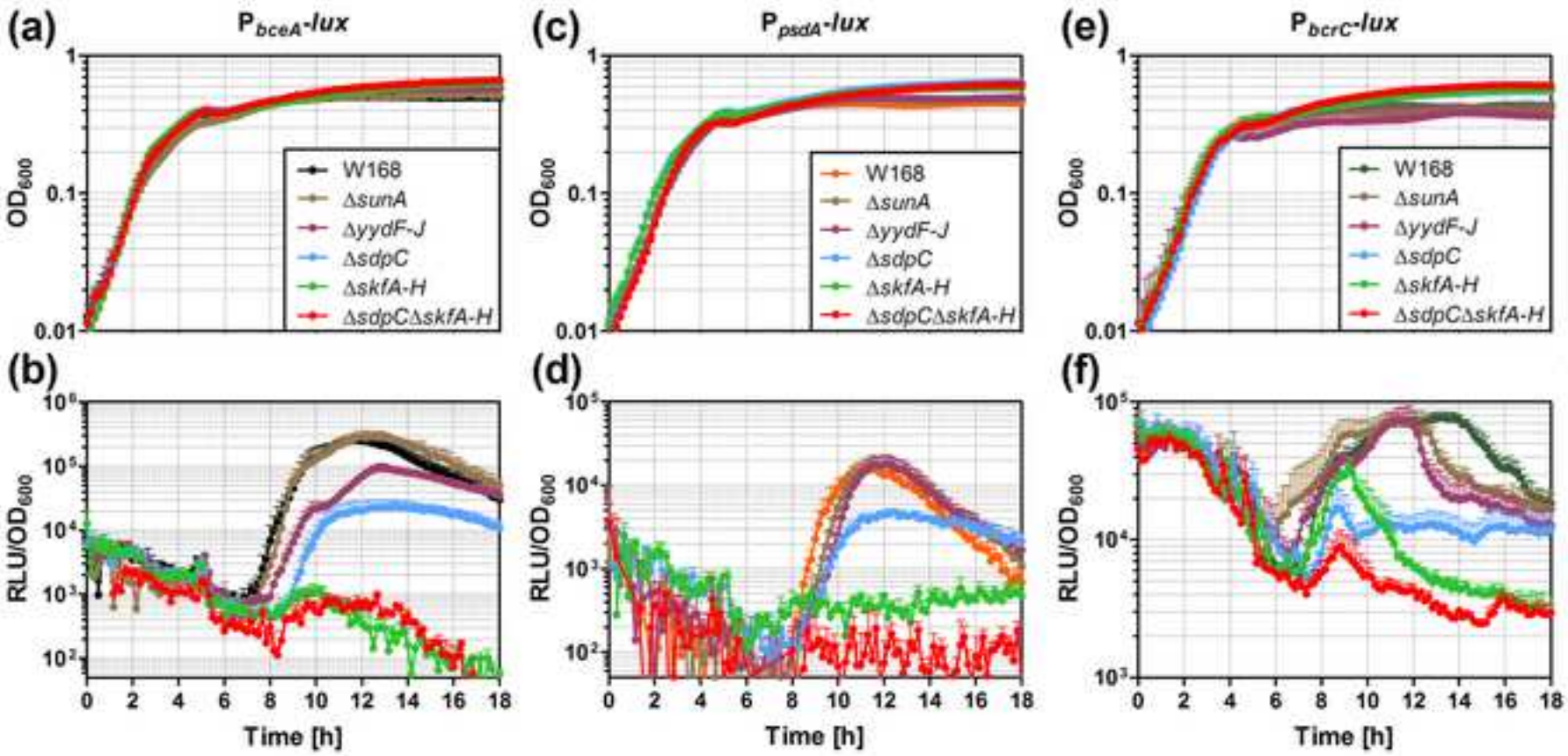

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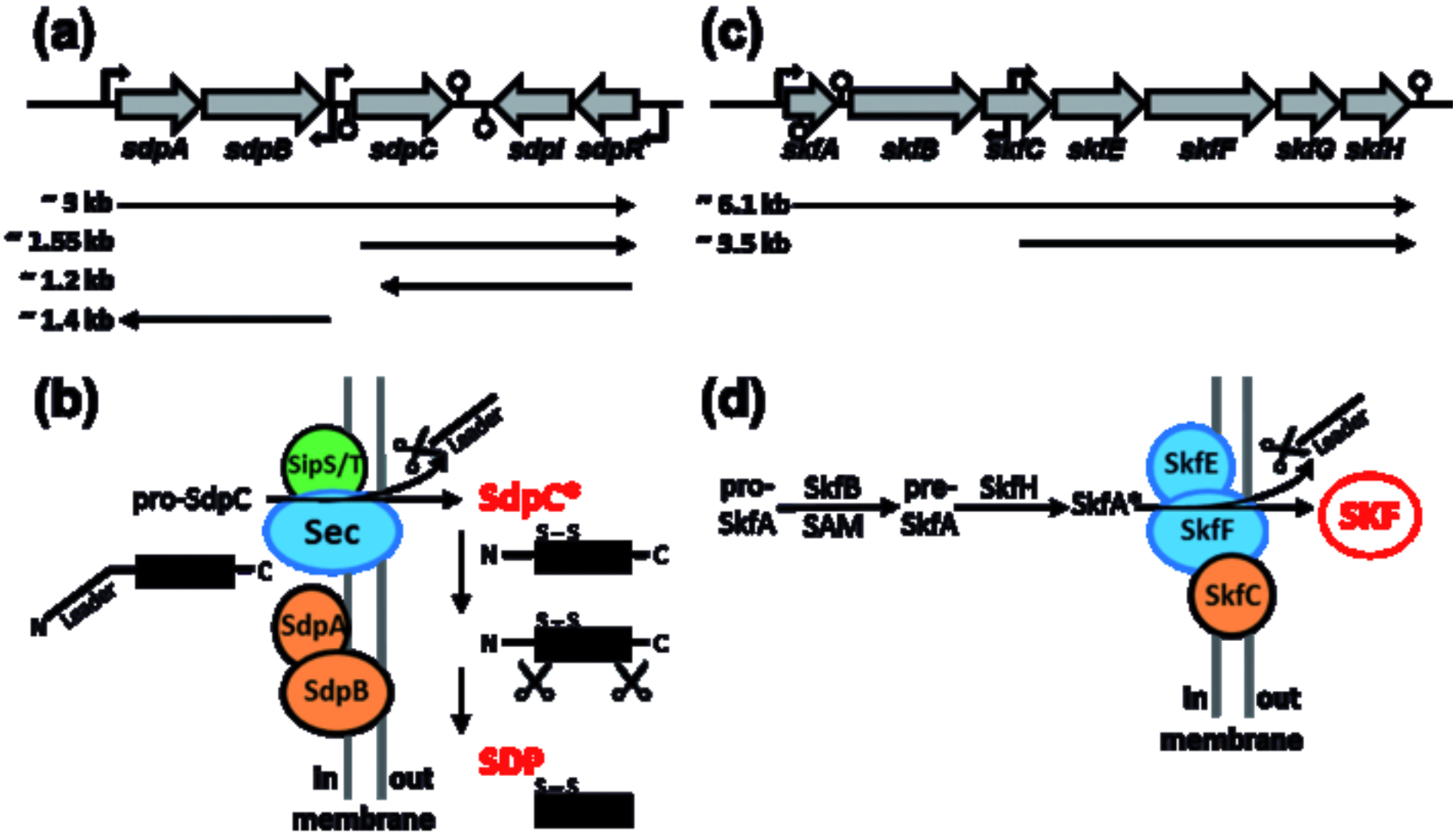

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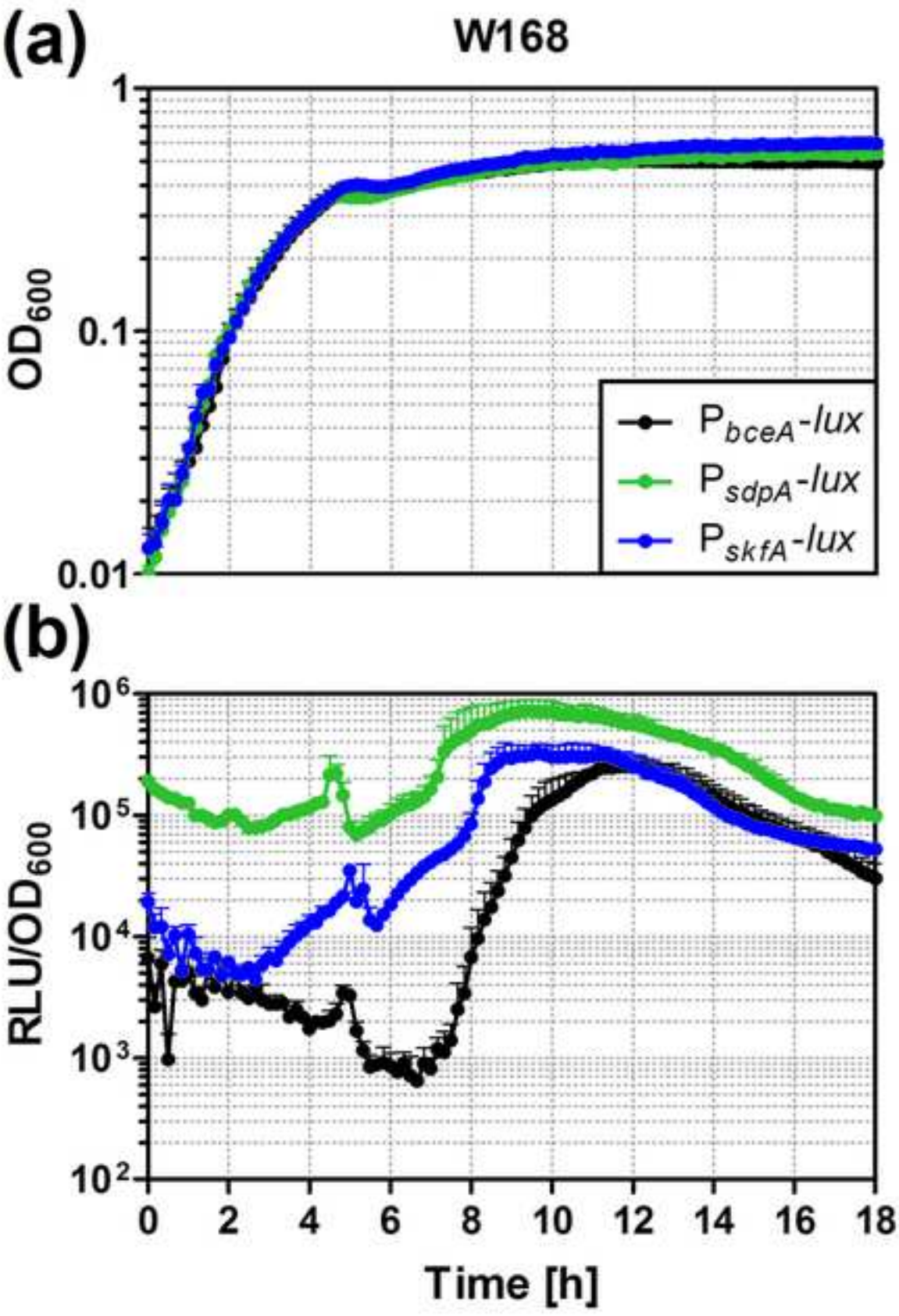

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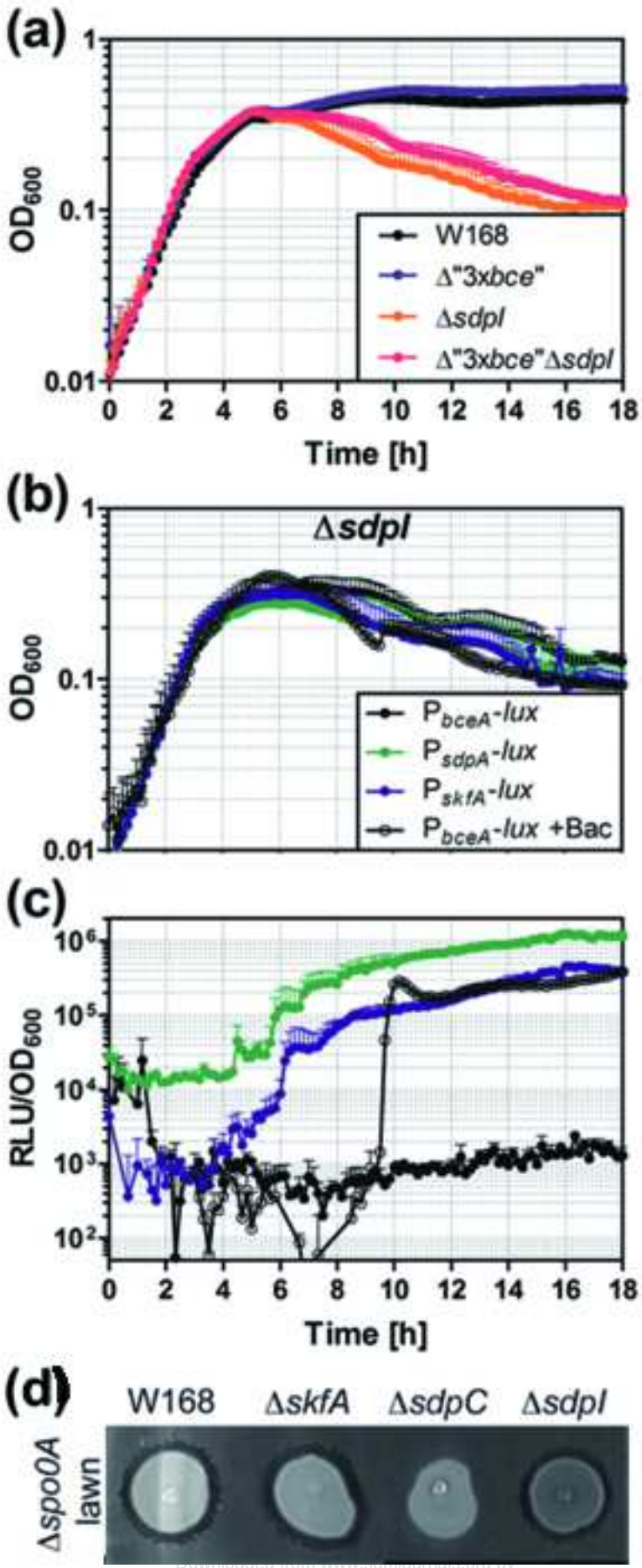

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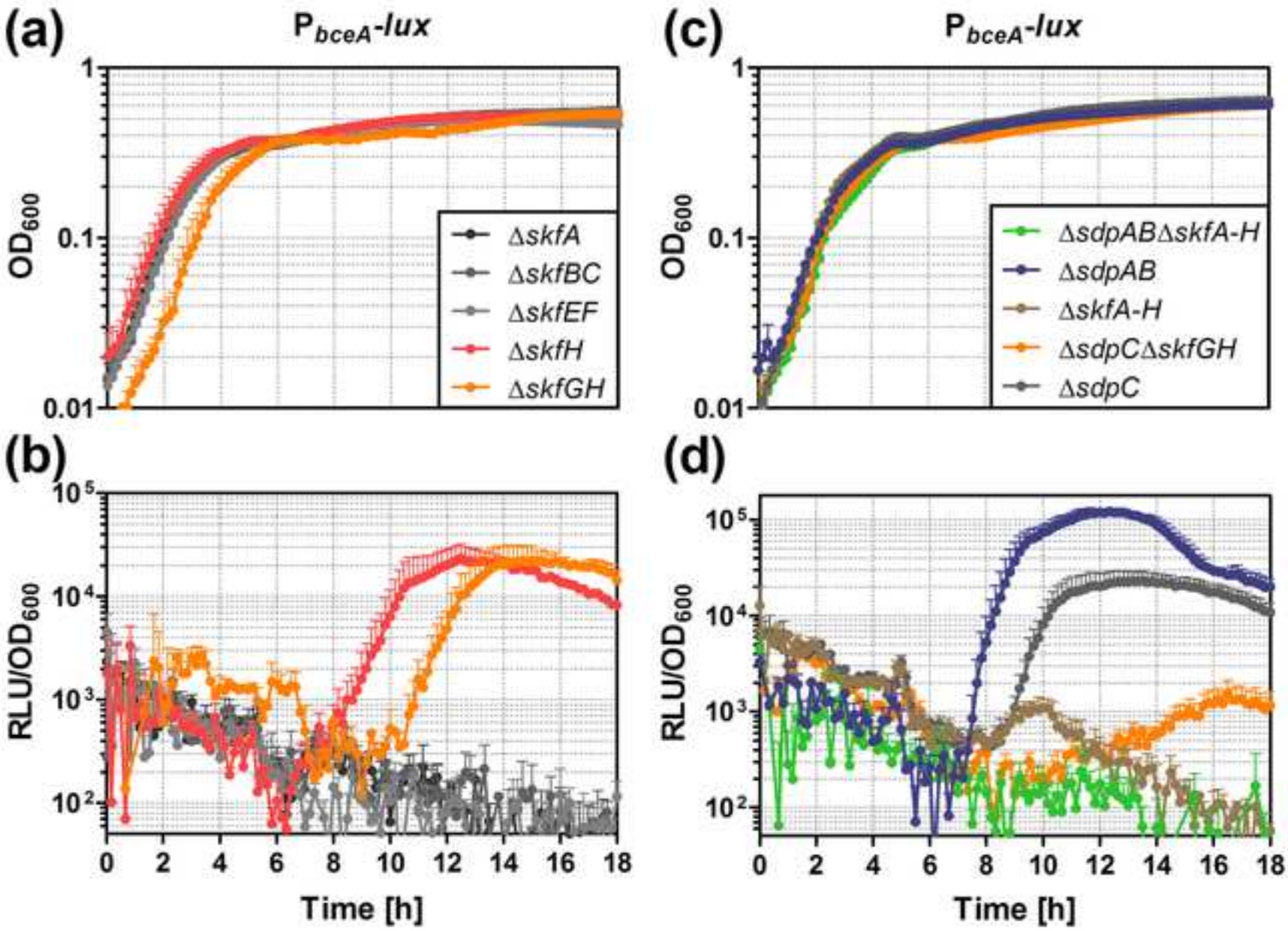

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